



## SEQUENCE LISTING

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Immusol Incorporated

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<130> 016556-003610US

<140> US 10/776,399

<141> 2004-02-10

<150> US 60/446,714

<151> 2003-02-11

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<170> PatentIn version 3.2

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 1 5 10 15

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 1 5 10 15

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 1 5 10 15



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<400> 239  
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<400> 240  
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<400> 244  
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1 5 10 15

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1 5 10 15

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 1 5 10 15

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<210> 264  
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 <212> PRT  
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<400> 264  
  
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 1 5 10 15

<210> 265  
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 <400> 265  
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<210> 266  
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 <212> PRT  
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<400> 266  
  
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 1 5 10 15

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<210> 268  
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 <212> PRT  
 <213> Homo sapiens

<400> 268  
  
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 1 5 10 15

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<210> 269
<211> 54
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<220>
<223> variant 1 semi-randomized oligonucleotide for tyrosine
      kinase family portion of catalytic domain

<220>
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<222> (1)..(1)
<223> n = c modified by 5' phosphate

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ncaggacgac aaaaagacht gygarggstg yaargghctt tttaggcttt tcgg          54

<210> 270
<211> 54
<212> DNA
<213> Artificial

<220>
<223> variant 2 semi-randomized oligonucleotide for tyrosine
      kinase family portion of catalytic domain

<220>
<221> modified_base
<222> (1)..(1)
<223> n = c modified by 5' phosphate

<220>
<221> modified_base
<222> (37)..(37)
<223> n = g, a, c, or t

<400> 270
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<210> 271
<211> 54
<212> DNA
<213> Artificial

<220>
<223> variant 3 semi-randomized oligonucleotide for tyrosine
      kinase family portion of catalytic domain

<220>
<221> modified_base
<222> (1)..(1)
<223> n = c modified by 5' phosphate

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<210> 272  
 <211> 53  
 <212> DNA  
 <213> Artificial  
  
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 <223> variant 4 semi-randomized oligonucleotide for tyrosine  
 kinase family portion of catalytic domain  
  
 <220>  
 <221> modified\_base  
 <222> (1)..(1)  
 <223> n = c modified by 5' phosphate  
  
 <400> 272  
 ncaggacgac aaaaagcctg cracggctgc wsmggycctt ttaggctttt cgg 53

<210> 273  
 <211> 54  
 <212> DNA  
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 <223> variant 5 semi-randomized oligonucleotide for tyrosine  
 kinase family portion of catalytic domain  
  
 <220>  
 <221> modified\_base  
 <222> (1)..(1)  
 <223> n = c modified by 5' phosphate  
  
 <400> 273  
 ncaggacgac aaaaagasct gtgayggstg caagggycct ttaggctttt tcgg 54

<210> 274  
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 <212> DNA  
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 kinase family portion of catalytic domain  
  
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 <221> modified\_base  
 <222> (1)..(1)  
 <223> n = c modified by 5' phosphate  
  
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 <221> modified\_base  
 <222> (18)..(18)  
 <223> n = g, a, c, or t  
  
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<210> 275  
 <211> 54  
 <212> DNA  
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 <223> variant 7 semi-randomized oligonucleotide for tyrosine  
 kinase family portion of catalytic domain  
  
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 <221> modified\_base  
 <222> (1)..(1)  
 <223> n = c modified by 5' phosphate  
  
 <220>  
 <221> modified\_base  
 <222> (19)..(19)  
 <223> n = g, a, c, or t  
  
 <400> 275  
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 <210> 276  
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 <212> DNA  
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 kinase family portion of catalytic domain  
  
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 <221> modified\_base  
 <222> (1)..(1)  
 <223> n = c modified by 5' phosphate  
  
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 <213> Artificial  
  
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 kinase family portion of catalytic domain  
  
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 <221> modified\_base  
 <222> (1)..(1)  
 <223> n = c modified by 5' phosphate  
  
 <400> 277  
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<210> 278  
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 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> adapter oligonucleotide Univ-1(FseI)  
  
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<210> 279  
 <211> 21  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> adapter oligonucleotide Univ-2(AscI)  
  
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 <222> (1)..(1)  
 <223> n = c modified by 5' phosphate  
  
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<210> 280  
 <211> 569  
 <212> DNA  
 <213> Artificial  
  
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 <223> human U6/murine U6 opposing promoter cassette  
  
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 catatacgat acaaggctgt tagagagata attagaatta atttgactgt aaacacaaag 120  
 atattagtac aaaatacgtg acgtagaaag taataatttc ttgggtagtt tgcagtttta 180  
 aaattatggt ttaaaatgga ctatcatatg cttaccgtaa cttgaaagta tttcgatttc 240  
 ttggctttat atatcggccg gcctcgaggc ggcctatatt tatagtctca aaacacacaa 300  
 ttactttaca gttaggggtga gtttcctttt gtgctgtttt ttaaaataat aatttagtat 360  
 ttgtatctct tatagaaatc caagcctatc atgtaaaatg tagctagtat taaaaagaac 420  
 agattatctg tcttttatcg cacattaagc ctctatagtt actaggaaat attatatgca 480  
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<210> 281
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<220>
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      (ZnF_C4 domain) consensus sequence (21 nt)

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<222> (1)..(21)
<223> n = g, a, c or t

<400> 281
dyntgyrrnr sntgywvvr b n
21

<210> 282
<211> 7
<212> PRT
<213> Artificial

<220>
<223> tyrosine kinase family portion of catalytic domain
      variant 1 signature motif

<400> 282
His Arg Asp Leu Lys Ser Ser
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<210> 283
<211> 7
<212> PRT
<213> Artificial

<220>
<223> tyrosine kinase family portion of catalytic domain
      variant 2 signature motif

<220>
<221> MOD_RES
<222> (4)
<223> Xaa = Leu, Val or Ile

<220>
<221> MOD_RES
<222> (6)
<223> Xaa = Ala or Val

<400> 283
His Arg Asx Xaa Ala Xaa Arg
  1             5

<210> 284
<211> 7
<212> PRT
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<220>  
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variant 3 signature motif

<220>  
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<223> Xaa = Ala or Ser

<400> 284

His Arg Asp Leu Arg Xaa Ala  
1 5

<210> 285  
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<220>  
<223> tyrosine kinase family portion of catalytic domain  
variant 4 signature motif

<220>  
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<223> Xaa = Arg or Lys

<400> 285

His Xaa Asp Leu Ala Thr Arg  
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<210> 286  
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<220>  
<223> tyrosine kinase family portion of catalytic domain  
variant 5 signature motif

<400> 286

His Arg Asp Leu Ala Ala Arg  
1 5

<210> 287  
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<220>  
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variant 6 signature motif

<400> 287

His Lys Asp Leu Ala Ala Arg  
1 5

<210> 288

<211> 7

<212> PRT

<213> Artificial

<220>

<223> tyrosine kinase family portion of catalytic domain  
variant 7 signature motif

<400> 288

His Arg Asp Ile Ala Ala Arg  
1 5

<210> 289

<211> 19

<212> DNA

<213> Artificial

<220>

<223> nuclear hormone receptor family zinc finger domain  
(ZnF\_C4 domain) consensus sequence (19 nt)

<220>

<221> modified\_base

<222> (1)..(19)

<223> n = g, a, c or t

<400> 289

dyntgyrrnr sntgywvvr

19

<210> 290

<211> 21

<212> DNA

<213> Artificial

<220>

<223> tyrosine kinase family portion of catalytic domain  
variant 1 consensus sequence

<400> 290

caccgsgacc tyaagtccag c

21

<210> 291

<211> 21

<212> DNA

<213> Artificial

<220>

<223> tyrosine kinase family portion of catalytic domain  
variant 2 consensus sequence

<400> 291  
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<210> 292  
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<220>  
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 variant 3 consensus sequence

<220>  
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 <222> (9)  
 <223> n = g, a, c or t

<400> 292  
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<210> 293  
 <211> 21  
 <212> DNA  
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<220>  
 <223> tyrosine kinase family portion of catalytic domain  
 variant 4 consensus sequence

<400> 293  
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<210> 294  
 <211> 21  
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<220>  
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 variant 5 consensus sequence

<220>  
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 <223> n = g, a, c or t

<400> 294  
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<210> 295  
 <211> 21  
 <212> DNA  
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<220>  
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 variant 6 consensus sequence

<400> 295  
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<210> 296  
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<220>  
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 variant 7 consensus sequence

<400> 296  
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<210> 297  
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<220>  
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 (ZnF\_C4 domain) variant 1 signature motif

<400> 297  
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<210> 298  
 <211> 21  
 <212> DNA  
 <213> Artificial

<220>  
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 (ZnF\_C4 domain) variant 1 consensus sequence

<400> 298  
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<210> 299  
 <211> 7  
 <212> PRT  
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<220>  
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 (ZnF\_C4 domain) variant 2 signature motif

<400> 299  
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<210> 300  
 <211> 21  
 <212> DNA  
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 (ZnF\_C4 domain) variant 2 consensus sequence  
  
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 (ZnF\_C4 domain) variant 3 signature motif  
  
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 <210> 302  
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 (ZnF\_C4 domain) variant 3 consensus sequence  
  
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 <210> 303  
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 (ZnF\_C4 domain) variant 4 signature motif  
  
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 Ala Cys Asx Gly Cys Ser Gly  
 1 5

<210> 304  
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 (ZnF\_C4 domain) variant 4 consensus sequence  
  
 <400> 304  
 gcctgcracg gctgcwsmgg y 21  
  
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 (ZnF\_C4 domain) variant 5 signature motif  
  
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 <223> Xaa = Thr or Ser  
  
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 Xaa Cys Asp Gly Cys Lys Gly  
 1 5  
  
 <210> 306  
 <211> 21  
 <212> DNA  
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 (ZnF\_C4 domain) variant 5 consensus sequence  
  
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 <210> 307  
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 <212> PRT  
 <213> Artificial  
  
 <220>  
 <223> nuclear hormone receptor family zinc finger domain  
 (ZnF\_C4 domain) variant 6 signature motif  
  
 <400> 27  
  
 Ala Cys Glu Gly Cys Lys Gly  
 1 5



<210> 308  
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 <213> Artificial

<220>  
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 (ZnF\_C4 domain) variant 6 consensus sequence

<220>  
 <221> modified\_base  
 <222> (3)  
 <223> n = g, a, c or t

<400> 308  
 gcntgygarg gvtgyaagg y

21

<210> 309  
 <211> 7  
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<220>  
 <223> nuclear hormone receptor family zinc finger domain  
 (ZnF\_C4 domain) variant 7 signature motif

<220>  
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<400> 309

Thr Cys Glu Xaa Cys Lys Gly  
 1 5

<210> 310  
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<220>  
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 (ZnF\_C4 domain) variant 7 consensus sequence

<220>  
 <221> modified\_base  
 <222> (3)  
 <223> n = g, a, c or t

<400> 310  
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21

<210> 311  
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<220>  
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 (ZnF\_C4 domain) variant 8 signature motif  
 <400> 311

Thr Cys Gly Ser Cys Lys Val  
 1 5

<210> 312  
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<220>  
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 (ZnF\_C4 domain) variant 8 consensus sequence

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21

<210> 313  
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<220>  
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 (ZnF\_C4 domain) variant 9 signature motif

<220>  
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<400> 313

Ser Cys Glu Xaa Cys Lys Ala  
 1 5

<210> 314  
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<220>  
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 (ZnF\_C4 domain) variant 9 consensus sequence

<400> 314  
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21